

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/680,963A  
Source: IEWO  
Date Processed by STIC: 5-26-05

# ENTERED



IFWO

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/680,963A**

**DATE: 05/26/2005**  
**TIME: 10:30:14**

**Input Set : A:\GFI-108 Sequence listing.ST25**  
**Output Set: N:\CRF4\05262005\J680963A.raw**

3 <110> APPLICANT: GlycoFi, Inc.  
 4 Bobrowicz, Piotr  
 5 Hamilton, Stephen R.  
 6 Gerngross, Tilman U.  
 7 Wildt, Stefan  
 8 Choi, Byung-Kwon  
 9 Nett, Juergen H.  
 10 Davidson, Robert C.  
 12 <120> TITLE OF INVENTION: N-Acetylglucosaminyltransferase III expression in lower  
 13 eukaryotes  
 15 <130> FILE REFERENCE: GFI-108 CIP  
 17 <140> CURRENT APPLICATION NUMBER: US 10/680,963A  
 18 <141> CURRENT FILING DATE: 2003-10-07  
 20 <150> PRIOR APPLICATION NUMBER: US 10/371,877  
 21 <151> PRIOR FILING DATE: 2003-02-20  
 23 <150> PRIOR APPLICATION NUMBER: US 09/892,591  
 24 <151> PRIOR FILING DATE: 2001-06-27  
 26 <150> PRIOR APPLICATION NUMBER: US 60/214,358  
 27 <151> PRIOR FILING DATE: 2000-06-28  
 29 <150> PRIOR APPLICATION NUMBER: US 60/215,638  
 30 <151> PRIOR FILING DATE: 2000-06-30  
 32 <150> PRIOR APPLICATION NUMBER: US 60/279,997  
 33 <151> PRIOR FILING DATE: 2001-03-30  
 35 <150> PRIOR APPLICATION NUMBER: PCT/US02/41510  
 36 <151> PRIOR FILING DATE: 2002-12-24  
 38 <150> PRIOR APPLICATION NUMBER: US 60/344,169  
 39 <151> PRIOR FILING DATE: 2001-12-27  
 41 <160> NUMBER OF SEQ ID NOS: 101  
 43 <170> SOFTWARE: PatentIn version 3.2  
 45 <210> SEQ ID NO: 1  
 W--> 46 <400> SEQUENCE: 1  
 W--> 47 000  
 50 <210> SEQ ID NO: 2  
 W--> 51 <400> SEQUENCE: 2  
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 56 <211> LENGTH: 21  
 57 <212> TYPE: DNA  
 58 <213> ORGANISM: artificial  
 60 <220> FEATURE:  
 61 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,6-mannosyltransferase)  
 63 <400> SEQUENCE: 3  
 64 atggcgaagg cagatggcag t

(pg. 6)

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Input Set : A:\GFI-108 Sequence listing.ST25  
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67 <210> SEQ ID NO: 4
68 <211> LENGTH: 21
69 <212> TYPE: DNA
70 <213> ORGANISM: artificial
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,6-
mannosyltransferase)
75 <400> SEQUENCE: 4
76 ttatcccttc caacttcctt c 21
79 <210> SEQ ID NO: 5
80 <211> LENGTH: 26
81 <212> TYPE: DNA
82 <213> ORGANISM: artificial
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,2
86 mannosyltransferases)
89 <220> FEATURE:
90 <221> NAME/KEY: misc_feature
91 <222> LOCATION: (9)..(9)
92 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
94 <220> FEATURE:
95 <221> NAME/KEY: misc_feature
96 <222> LOCATION: (12)..(12)
97 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
99 <220> FEATURE:
100 <221> NAME/KEY: misc_feature
101 <222> LOCATION: (18)..(18)
102 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
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W--> 105 taytggmng tngarcyna yathaa 26
108 <210> SEQ ID NO: 6
109 <211> LENGTH: 20
110 <212> TYPE: DNA
111 <213> ORGANISM: artificial
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,2
115 mannosyltransferases)
118 <220> FEATURE:
119 <221> NAME/KEY: misc_feature
120 <222> LOCATION: (6)..(6)
121 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
123 <220> FEATURE:
124 <221> NAME/KEY: misc_feature
125 <222> LOCATION: (12)..(12)
126 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
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W--> 129 gcrtcncccc anckytcrrta 20
132 <210> SEQ ID NO: 7
W--> 133 <400> SEQUENCE: 7
W--> 134 000

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Input Set : A:\GFI-108 Sequence listing.ST25  
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137 <210> SEQ ID NO: 8
W--> 138 <400> SEQUENCE: 8
W--> 139 000
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143 <211> LENGTH: 458
144 <212> TYPE: PRT
145 <213> ORGANISM: Saccharomyces cerevisiae
147 <400> SEQUENCE: 9
149 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
150 1 5 10 15
153 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
154 20 25 30
157 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
158 35 40 45
161 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
162 50 55 60
165 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
166 65 70 75 80
169 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
170 85 90 95
173 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
174 100 105 110
177 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
178 115 120 125
181 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
182 130 135 140
185 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
186 145 150 155 160
189 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
190 165 170 175
193 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
194 180 185 190
197 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
198 195 200 205
201 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
202 210 215 220
205 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
206 225 230 235 240
209 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
210 245 250 255
213 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
214 260 265 270
217 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
218 275 280 285
221 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
222 290 295 300
225 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
226 305 310 315 320
229 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His

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```

230           325           330           335
233 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
234           340           345           350
237 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
238           355           360           365
241 Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
242           370           375           380
245 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
246 385           390           395           400
249 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
250           405           410           415
253 Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Ala
254           420           425           430
257 Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
258           435           440           445
261 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
262           450           455
265 <210> SEQ ID NO: 10
266 <211> LENGTH: 458
267 <212> TYPE: PRT
268 <213> ORGANISM: Saccharomyces cerevisiae
270 <400> SEQUENCE: 10
272 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
273 1           5           10           15
276 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
277           20           25           30
280 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
281           35           40           45
284 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
285           50           55           60
288 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
289 65           70           75           80
292 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
293           85           90           95
296 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
297           100          105          110
300 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
301           115          120          125
304 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
305           130          135          140
308 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
309 145           150           155           160
312 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
313           165           170           175
316 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
317           180           185           190
320 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
321           195           200           205
324 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu

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325	210	215	220													
328	Leu	Tyr	Phe	Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala
329	225		230		235		240									
332	Asn	Val	Ile	Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln
333			245		250		255									
336	Val	Ala	Val	Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu
337			260		265		270									
340	His	Cys	Ala	Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile
341			275		280		285									
344	Asn	Trp	Gln	Met	Met	Asp	Glu	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe	His
345			290		295		300									
348	Leu	Ala	Leu	Leu	Ile	Ser	His	Leu	Ile	Ala	Leu	Thr	Thr	Leu	Phe	Val
349	305		310		315		320									
352	Thr	Arg	Tyr	Pro	Arg	Ile	Leu	Pro	Asp	Leu	Trp	Ser	Ser	Leu	Cys	His
353			325		330		335									
356	Pro	Leu	Arg	Lys	Asn	Ala	Val	Leu	Asn	Ala	Asn	Pro	Ala	Lys	Thr	Ile
357			340		345		350									
360	Pro	Phe	Val	Leu	Ile	Ala	Ser	Asn	Phe	Ile	Gly	Val	Leu	Phe	Ser	Arg
361			355		360		365									
364	Ser	Leu	His	Tyr	Gln	Phe	Leu	Ser	Trp	Tyr	His	Trp	Thr	Leu	Pro	Ile
365			370		375		380									
368	Leu	Ile	Phe	Trp	Ser	Gly	Met	Pro	Phe	Phe	Val	Gly	Pro	Ile	Trp	Tyr
369	385		390		395		400									
372	Val	Leu	His	Glu	Trp	Cys	Trp	Asn	Ser	Tyr	Pro	Pro	Asn	Ser	Gln	Ala
373			405		410		415									
376	Ser	Thr	Leu	Leu	Leu	Ala	Leu	Asn	Thr	Val	Leu	Leu	Leu	Leu	Leu	Ala
377			420		425		430									
380	Leu	Thr	Gln	Leu	Ser	Gly	Ser	Val	Ala	Leu	Ala	Lys	Ser	His	Leu	Arg
381			435		440		445									
384	Thr	Thr	Ser	Ser	Met	Glu	Lys	Lys	Leu	Asn						
385			450		455											
388	<210>	SEQ	ID	NO:	11											
389	<211>	LENGTH:	389													
390	<212>	TYPE:	PRT													
391	<213>	ORGANISM:	Saccharomyces cerevisiae													
393	<400>	SEQUENCE:	11													
395	Trp	Gln	Asp	Leu	Lys	Asp	Gly	Val	Arg	Tyr	Val	Ile	Phe	Asp	Cys	Arg
396	1				5			10				15				
399	Ala	Asn	Leu	Ile	Val	Met	Pro	Leu	Leu	Ile	Leu	Phe	Glu	Ser	Met	Leu
400					20			25			30					
403	Cys	Lys	Ile	Ile	Ile	Lys	Lys	Val	Ala	Tyr	Thr	Glu	Ile	Asp	Tyr	Lys
404					35			40			45					
407	Ala	Tyr	Met	Glu	Gln	Ile	Glu	Met	Ile	Gln	Leu	Asp	Gly	Met	Leu	Asp
408					50			55			60					
411	Tyr	Ser	Gln	Val	Ser	Gly	Gly	Thr	Gly	Pro	Leu	Val	Tyr	Pro	Ala	Gly
412					65			70			75			80		
415	His	Val	Leu	Ile	Tyr	Lys	Met	Met	Tyr	Trp	Leu	Thr	Glu	Gly	Met	Asp
416					85			90			95					
419	His	Val	Glu	Arg	Gly	Gln	Val	Phe	Phe	Arg	Tyr	Leu	Tyr	Leu	Leu	Thr

RAW SEQUENCE LISTING ERROR SUMMARY                   DATE: 05/26/2005  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 9,12,18  
Seq#:6; N Pos. 6,12  
Seq#:75; N Pos. 17,20

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,41,42,47,48,49,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68  
Seq#:69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,94,95,96  
Seq#:97,98,99,100,101

**VERIFICATION SUMMARY**

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Input Set : A:\GFI-108 Sequence listing.ST25  
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L:46 M:283 W: Missing Blank Line separator, <400> field identifier  
L:47 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (1) SEQUENCE:  
L:51 M:283 W: Missing Blank Line separator, <400> field identifier  
L:52 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (2) SEQUENCE:  
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
L:133 M:283 W: Missing Blank Line separator, <400> field identifier  
L:134 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:  
L:138 M:283 W: Missing Blank Line separator, <400> field identifier  
L:139 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:  
L:2445 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2446 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (43) SEQUENCE:  
L:2450 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2451 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:  
L:3240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0